

A new parasitic barnacle (Crustacea, Cirripedia, Rhizocephala, *Mycetomorpha*) from the abyssal zone in the northwestern Pacific

Keiichi Kakui¹

¹ Department of Biological Sciences, Faculty of Science, Hokkaido University, Sapporo 060-0810, Japan

<https://zoobank.org/C325C2A4-0279-43F5-B7C1-FB5B60D277F5>

Corresponding author: Keiichi Kakui (kakui@eis.hokudai.ac.jp)

Academic editor: K. von Rintelen ♦ Received 14 February 2024 ♦ Accepted 19 March 2024 ♦ Published 3 April 2024

Abstract

I describe the parasitic barnacle *Mycetomorpha abyssalis* **sp. nov.** from the crangonid shrimp *Sclerocrangon zenkevitchi* collected from 3893–3890 m depth off the eastern coast of Iwate, Japan, northwestern Pacific. This is the first *Mycetomorpha* rhizocephalan from the abyssal zone and the third species in *Mycetomorpha*. *Mycetomorpha abyssalis* **sp. nov.** differs from its congeners *M. vancouverensis* and *M. albatrossi* in (1) triangular shield lacking, (2) stalk one-quarter of length from posterior end of externa, (3) mantle opening clearly anterior to stalk, (4) different host genus, and (5) depth range much deeper. I determined partial sequences for the mitochondrial cytochrome *c* oxidase subunit I (COI) and 16S rRNA genes and nuclear 18S rRNA and 28S rRNA genes from *M. abyssalis* **sp. nov.** for future DNA barcoding and phylogeny. Kimura 2-parameter distances between *M. abyssalis* **sp. nov.** and *M. vancouverensis* were 21.2% (16S), 0.6% (18S), and 1.5% (28S).

Key Words

Caridea, deep sea, integrative taxonomy, mesoparasite, parasite, turbo taxonomy

Introduction

Mycetomorpha Potts, 1912, the sole genus in the rhizocephalan barnacle family Mycetomorphidae, contains the two species *Mycetomorpha vancouverensis* Potts, 1912 and *Mycetomorpha albatrossi* Høeg & Rybakov, 1996 (Høeg and Rybakov 1996). These utilize crangonid shrimps as hosts and have been reported only from the northern Pacific, at depths shallower than 300 m (Potts 1912; Butler 1955, 1980; Høeg and Rybakov 1996; Sloan et al. 2001; Wheeler and McIntosh 2021; Eibye-Jacobsen et al. 2024; GBIF 2024; Orrell and Informatics Office 2024) (Fig. 1). The two species differ in external morphology (Høeg and Rybakov 1996) and utilize host shrimps in different genera: *Neocrangon communis* (Rathbun, 1899) for *M. vancouverensis*; *Metacrangon variabilis* (Rathbun, 1902) and *Metacrangon acclivis* (Rathbun, 1902) for *M. albatrossi*. Molecular phylogenetic analyses (Høeg et al. 2020; Korn et al. 2020) have suggested that Mycetomorphidae is closely related to the family Peltogastridae.

Here I describe a new *Mycetomorpha* species based on one individual parasitic on the crangonid *Sclerocrangon zenkevitchi* Birshtein & Vinogradov, 1953 from the abyssal zone in the Japan Trench, northwestern Pacific. This is the first abyssal record for *Mycetomorpha*. Additionally, I provide partial sequences for its cytochrome *c* oxidase subunit I (COI), 16S rRNA, 18S rRNA, and 28S rRNA genes for DNA barcoding and future phylogenetic analyses.

Methods

The host shrimp *Sclerocrangon zenkevitchi* (identified by Tomoyuki Komai; Natural History Museum and Institute, Chiba) was collected with a beam trawl on 29 September 2023 during cruise KH-23-5 of R/V *Hakuho-maru* (Japan Agency for Marine-Earth Science and Technology; JAMSTEC), at Station F2 (39°28.555'N, 143°47.347'E to 39°27.934'N, 143°47.240'E), depth 3893–3890 m. The fresh shrimp was photographed.

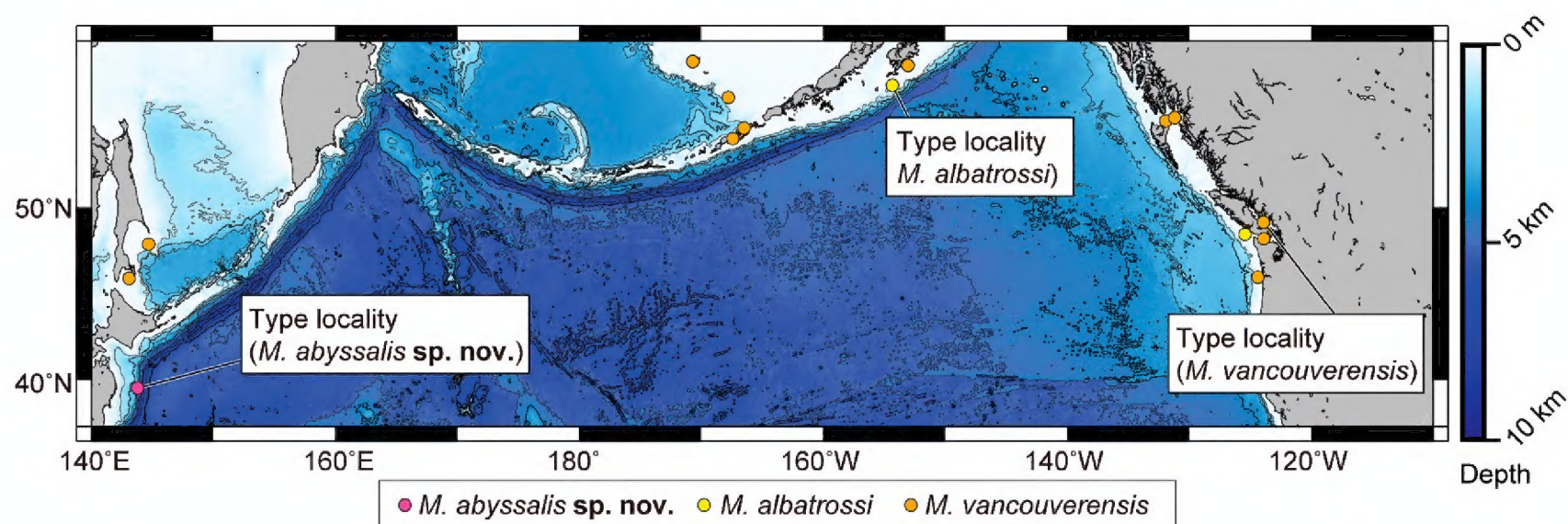


Figure 1. Map showing the global distribution of *Mycetomorpha*. Bathymetric contour intervals are 1000 m, with thicker contour lines every 2000 m. The map and plots were generated with GMT6 software (Wessel et al. 2019) based on data publicly available from ETOPO1 (Amante and Eakins 2009; NOAA National Geophysical Data Center 2009).

Pleonite 1 bearing the parasite was removed from the body with scissors and placed in a petri dish. Soft tissue from host pleonite 1 was recovered, and fixed and preserved in 99% ethanol. The pleonite-1 exoskeleton penetrated by the parasite stalk was photographed. The parasite and surrounding pleonite-1 exoskeleton were removed and photographed. Some lobes of the parasite were detached, and fixed and preserved in 99% ethanol. The remaining portions of the host and parasite were fixed and preserved in 80% ethanol. The fixed parasite was observed with a Nikon SMZ1500 stereomicroscope; it was not sectioned, in order to retain the option for future non-destructive observation. The material examined in this study is deposited in the Natural History Museum and Institute, Chiba, Japan, catalogued under the acronym CBM-ZC.

The terms for orientation (anterior, posterior, left, right, dorsal, ventral) used herein for the parasite's externa correspond to those for the host ("dorsal" herein corresponds to the "upper" or "stalk side" in Høeg and Rybakov 1996). Externa length was measured from the anterior to posterior ends, lobes excluded; externa width was measured at the widest portion, lobes excluded. The carapace length (cl) of the host was measured from the orbital margin to the midpoint of the posterodorsal margin of the carapace.

Total DNA was extracted from several lobes of the parasite and from pleonal muscle of the host shrimp by using a NucleoSpin Tissue XS Kit (Macherey–Nagel, Germany). For the COI gene, primers LCO1490 and HCO2198 (Folmer et al. 1994) were used for PCR amplification and cycle sequencing (CS). For the 16S gene, primers 16sar-L and 16sbr-H (Palumbi et al. 2002) were used for amplification and CS. For the 18S gene, primers SR1 and SR12 (Nakayama et al. 1996) were used for amplification, and primers SR3, 18S-b3F, 18S-b4F, 18S-b4R, 18S-a4R, 18S-b5F, 18S-b6F, 18S-a6R, and 18S-b8F (Nakayama et al. 1996; Kakui et al. 2011, 2021; Kakui and Shimada 2017, 2022; Kakui and Hiruta 2022) for CS. For the 28S gene, primers 300F and L1642 (Lockyer et al. 2003) were used for amplification, and primers 28S-Rd4.2b, 300F, 900F, and U1148 (Whiting 2002; Lockyer et al. 2003) for CS. Amplification conditions for COI and 16S with TaKaRa Ex Taq DNA polymerase (TaKaRa Bio, Japan) were

94 °C for 1 min; 35 cycles of 98 °C for 10 s, 50 °C (COI) or 42 °C (16S) for 30 s, and 72 °C for 50 s; and 72 °C for 2 min. Conditions for 18S and 28S with KOD FX Neo (Toyobo, Japan) were 94 °C for 2 min; 45 cycles of 98 °C for 10 s, 65 °C (18S) or 52 °C (28S) for 30 s, and 68 °C for 75 s; and 68 °C for 3 min. All nucleotide sequences were determined with a BigDye Terminator Kit ver. 3.1 and 3730 DNA Analyzer (Life Technologies, USA). Fragments were concatenated by using MEGA7 (Kumar et al. 2016). The sequences determined in this study were deposited in the International Nucleotide Sequence Database (INSD) through the DNA Data Bank of Japan (DDBJ).

The 16S, 18S, and 28S sequences from the new species were aligned individually with homologs from *M. vancouverensis* (16S, 534 bp, MH974513; 18S, 1757 bp, MH974514; 28S, 682 bp, MH974515; Høeg et al. 2019) by using MUSCLE (Edgar 2004) and trimmed to the shortest length between them (16S, 494 bp; 18S, 1757 bp; 28S, 683 bp) after alignment. Kimura's (1980) 2-parameter (K2P) distance between the two species was calculated with MEGA7 for each gene.

Taxonomy

Family Mycetomorphidae Høeg & Rybakov, 1992

New Japanese name: ミノフクロムシ科 (Mino-fukuromushi-ka)

Genus *Mycetomorpha* Potts, 1912

New Japanese name: ミノフクロムシ属 (Mino-fukuromushi-zoku)

Mycetomorpha abyssalis sp. nov.

<https://zoobank.org/9C0FBC4F-5779-4100-BDC9-8D585C1A4160>

Figs 2–4

New Japanese name: メイフノミノフクロムシ (Meifu-no-mino-fukuromushi)

Etymology. The specific name *abyssalis* (Latin: abyssal) is an adjective referring to the collection of this species from an abyssal depth.

Type host. *Sclerocrangon zenkevitchi* Birshtein & Vinogradov, 1953 (Decapoda: Caridea: Crangonidae).

Attachment site. Pleonite 1 sternite.

Type locality. Off the eastern coast of Iwate, Japan, northwestern Pacific (39°28.555'N, 143°47.347'E to 39°27.934'N, 143°47.240'E), depth 3893–3890 m.

Material examined. Holotype, female (CBM-ZC 17789), one vial, ex. *S. zenkevitchi* (cl 26.7 mm; CBM-ZC 17788), collected on 29 September 2023 at the type

locality, R/V *Hakuho-maru* cruise KH-23-5, coll. by Keiichi Kakui.

Representative DNA sequences. One sequence each was determined from the holotype (CBM-ZC 17789) for COI (INSID accession number LC799150; 637 bp, encoding 212 amino acids), 16S (LC799151; 490 bp), 18S (LC799152; 1826 bp), and 28S (LC799153; 1169 bp).



Figure 2. *Mycetomorpha abyssalis* sp. nov., holotype, attached to the host, *Sclerocrangon zenkevitchi* Birshtein & Vinogradov, 1953, fresh specimen. Scale bar: 10 mm.

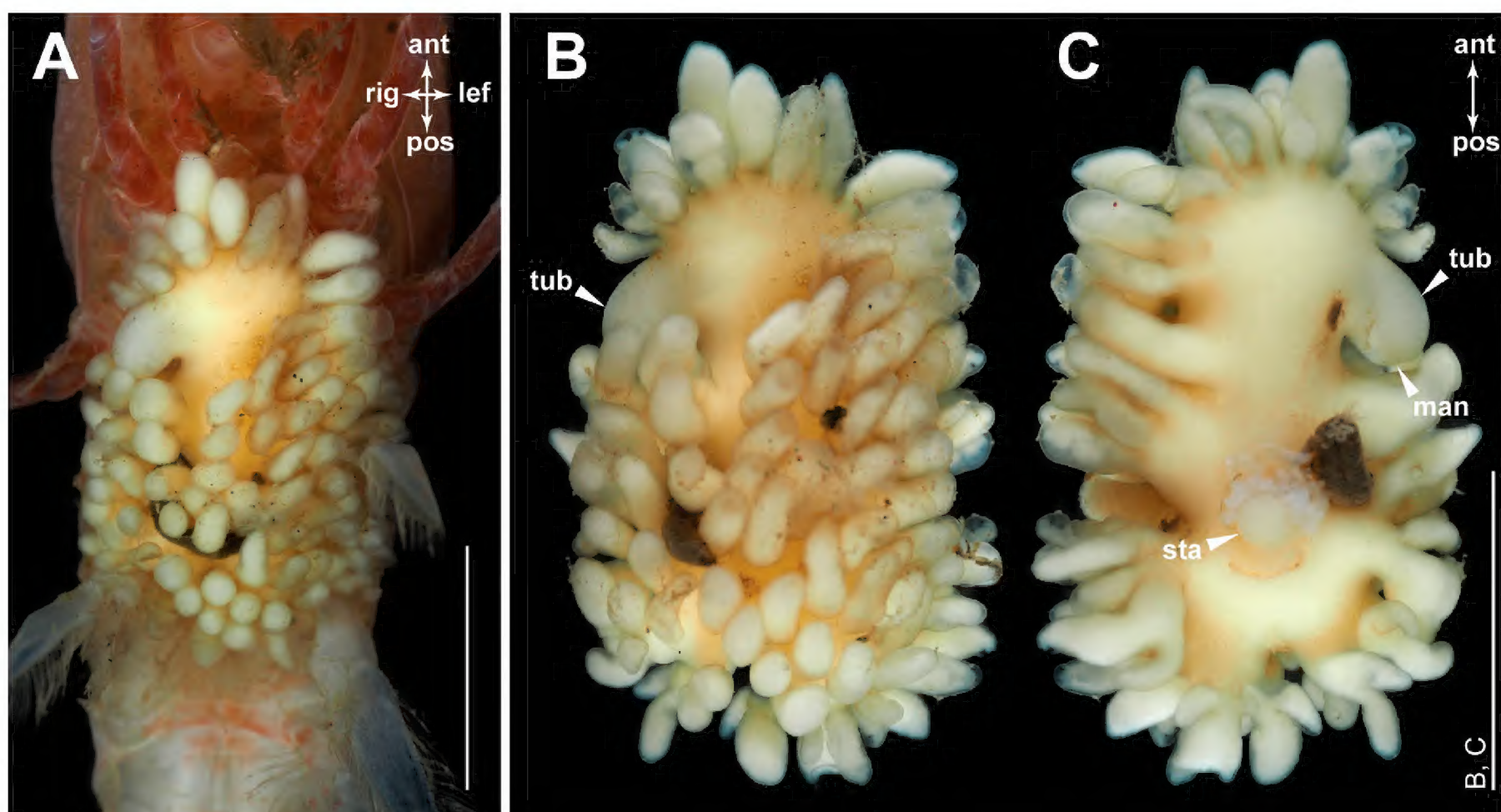


Figure 3. *Mycetomorpha abyssalis* sp. nov., holotype, fresh specimen. **A.** Habitus, parasitic on the host, ventral view; **B, C.** Habitus, ventral (**B**) and dorsal (**C**) views; **ant** – anterior; **lef** – left; **man** – mantle opening; **rig** – right; **pos** – posterior; **sta** – stalk; **tub** – tubular lobe. Scale bars: 10 mm.

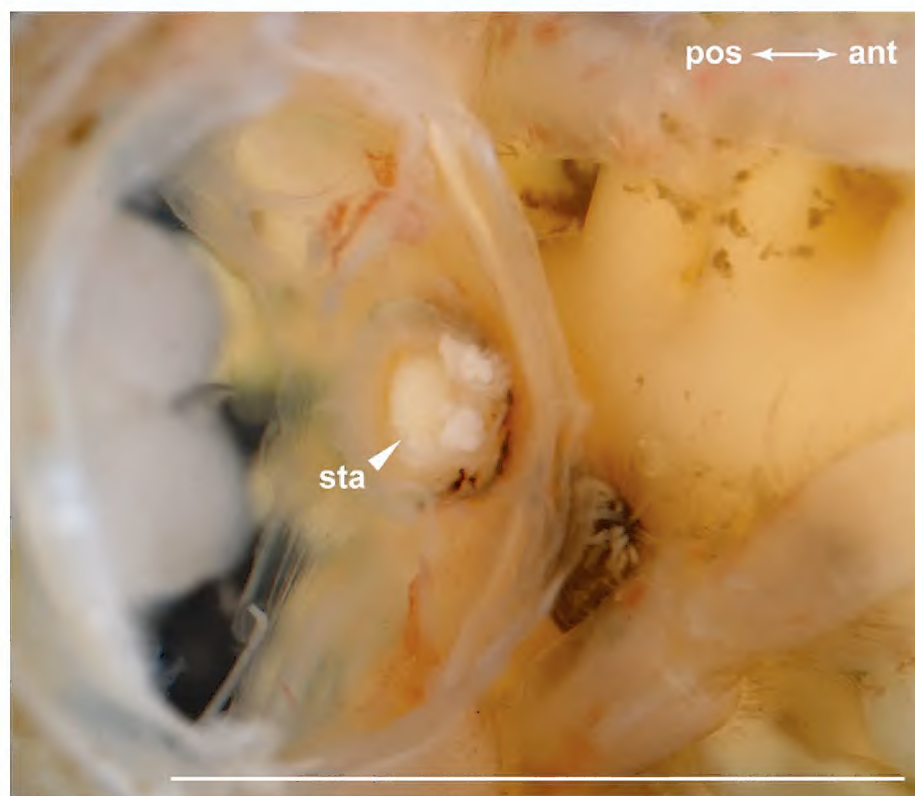


Figure 4. *Mycetomorpha abyssalis* sp. nov., holotype, showing stalk penetrating the host pleonite-1 sternite (soft tissue in pleonite 1 removed), anterodorsal view; no triangular shield observed. **ant** – anterior; **pos** – posterior; **sta** – stalk. Scale bar: 10 mm.

One sequence each was determined from the host (CBMZC 17788) for COI (LC799154; 658 bp, encoding 219 amino acids) and 18S (LC799155; 1846 bp).

Description of female holotype. Externa (Figs 2, 3) 16.6 mm in length, thinner than broad, a little over twice as long as maximum width (8.1 mm), rounded at ends, pale yellow (faded in ethanol, slightly yellowish); except dorsal and anteroventral regions, externa surface covered with short lobes; filled with developing embryos. Root system not observed. Stalk short, cylindrical, at one-quarter of length from posterior end of externa. Triangular shield lacking (Figs 3C, 4). Anterior, middle, and ventral lobes short, and ovoid or digitiform; posterior lobes short and branched. Tubular lobe anterior to stalk, at one-fifth of length from anterior end of externa, arising from right margin of externa, with mantle opening at tip; mantle opening anterior to stalk.

Distribution. Presently known only from the type locality.

Discussion

Mycetomorpha abyssalis sp. nov. is the third species described in this genus. The three congeners are morphologically similar to one another, but *M. abyssalis* sp. nov. differs from the others in (1) lacking a triangular shield (present in *M. vancouverensis*), (2) the location of the stalk at one-quarter the length from the posterior end of the externa (one-third in *M. albatrossi*), and (3) the mantle opening clearly anterior to the stalk (to the right of the stalk in *M. vancouverensis*; slightly anterior to the stalk in *M. albatrossi*) (Potts 1912; Høeg and Rybakov 1996). However, because the shape of the externa can vary ontogenetically (e.g., the size of externa, the distribution and

size of lobes; cf. Høeg and Rybakov 1996: fig. 1), these morphological differences should be treated with caution.

The genus of host shrimps is different among three species: *M. vancouverensis*, *M. albatrossi*, and *M. abyssalis* sp. nov. utilize the crangonid genera *Neocrangon*, *Metacrangon*, and *Sclerocrangon*, respectively. The depth range of 3893–3890 m recorded for *M. abyssalis* sp. nov. is far deeper than for the others (240 m or shallower for *M. vancouverensis*; 291 m or shallower for *M. albatrossi*; Høeg and Rybakov 1996; Wheeler and McIntosh 2021). The known depth range for *S. zenkevitchi* (2995–4070 m; Komai and Komatsu 2009) does not overlap those for *N. communis* (16–1537 m; Komai and Komatsu 2009), *M. variabilis* (92–1271 m; Komai 2012), and *M. acclivis* (146.3–486.5 m; Rathbun 1902). These differences in host group and vertical distribution of parasites and hosts support the conclusion that the specimen from Japan is not conspecific with either *M. vancouverensis* or *M. albatrossi*.

I determined COI, 16S, 18S, and 28S sequences of *M. abyssalis* sp. nov., and sequences for the last three genes were available for *M. vancouverensis*. K2P distances between two species were 21.2% (16S), 0.6% (18S), and 1.5% (28S). Noever et al. (2016) found K2P distances for 16S between two *Briarosaccus* species (Rhizocephala, Peltogastridae) in the range of 4.3–4.6%, suggesting the above difference in 16S may correspond to interspecific variation. In a BLAST search (Altschul et al. 1990), the COI sequence most similar to my sequence was from the insect *Rhodopsalta cruentata* (Fabricius, 1775) ([MZ470333](#); identity score 73.85%, query cover 100%; Bator et al. 2021), a misleading result likely due to the lack of any congeneric COI sequences in INSD (cf. Kakui and Hiruta 2022). A BLAST search with the “Organism” option set to “Rhizocephala” selected *Sacculina granifera* Boschma, 1973 ([DQ059779](#); identity score 72.64%, query cover 98%; Gurney et al. 2006) as the most similar sequence, but again the identity score was low. If congeneric sequences become available, COI sequences, which seem to evolve faster than 16S sequences (cf. Noever et al. 2016; Jung et al. 2021), will likely be a useful tool for *Mycetomorpha* taxonomy.

Acknowledgments

I thank Shigeaki Kojima and Yasunori Kano for the opportunity to join R/V *Hakuho-maru* cruise KH-23-5, conducted as a part of the project “Comprehensive study of diversity and evolutionary mechanisms of deep-sea animals in trenches in the northwestern Pacific” supported by KAKENHI grant JP19H00999 from the Japan Society for the Promotion of Science (JSPS); Captain Naoto Sakai and the crew of R/V *Hakuho-maru*, technicians from Marine Work Japan and MOL Marine & Engineering, and researchers aboard for support in collecting; Tomoyuki Komai for identification of the host shrimp; Akito Ogawa for help in photography; Genki Ishiyama and Mako Nakao for help in map production; and Matthew H. Dick for

reviewing the manuscript and editing the English. This study was supported in part by the Atmosphere and Ocean Research Institute, The University of Tokyo, and KAKENHI grants JP19K06800 and JP22H02681 from JSPS.

References

- Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ (1990) Basic local alignment search tool. *Journal of Molecular Biology* 215(3): 403–410. [https://doi.org/10.1016/S0022-2836\(05\)80360-2](https://doi.org/10.1016/S0022-2836(05)80360-2)
- Amante C, Eakins BW (2009) ETOPO1 1 arc-minute global relief model: procedures, data sources and analysis. NOAA Technical Memorandum NESDIS NGDC-24. National Geophysical Data Center, Boulder, 19 pp.
- Bator J, Marshall DC, Hill KBR, Cooley JR, Leston A, Simon C (2021) Phylogeography of the endemic red-tailed cicadas of New Zealand (Hemiptera: Cicadidae: *Rhodopsalta*), and molecular, morphological and bioacoustical confirmation of the existence of Hudson's *Rhodopsalta microdora*. *Zoological Journal of the Linnean Society* 195(4): 1219–1244. <https://doi.org/10.1093/zoolinnean/zlab065>
- Birshtein YA, Vinogradov LG (1953) New data on the decapod crustacean fauna in the Bering Sea. *Zoologicheskii Zhurnal* 32: 215–228. [in Russian]
- Boschma H (1973) *Sacculina granifera* nov. spec., a rhizocephalan parasite of the crab *Portunus* (*Portunus*) *pelagicus* from the coast of Queensland. *Proceedings of the Koninklijke Nederlandse Akademie van Wetenschappen, Series C* 76: 313–318.
- Butler TH (1955) Re-discovery of the parasitic cirripede, *Mycetomorpha vancouverensis* Potts, in British Columbia waters. *The Journal of Parasitology* 41: 321. <https://doi.org/10.2307/3274218>
- Butler TH (1980) Shrimps of the Pacific coast of Canada. *Canadian Bulletin of Fisheries and Aquatic Sciences* 202: [i–x] 1–280.
- Edgar RC (2004) MUSCLE: Multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Research* 32(5): 1792–1797. <https://doi.org/10.1093/nar/gkh340>
- Eibye-Jacobsen D, Pavesi L, Schiøtte T, Sørensen MV, Olesen J (2024) NHMD Invertebrate Zoology Collection. Natural History Museum of Denmark. Occurrence dataset. <https://doi.org/10.15468/wodhis> [Accessed via GBIF.org on 2024-02-05]
- Fabricius IC (1775) *Systema Entomologiae, sistens insectorum classes, ordines, genera, species, adiectis synonymis, locis, descriptionibus, observationibus*. Officina Libraria Kortii, Flensbvirgi and Lipsiae, 832 pp. <https://doi.org/10.5962/bhl.title.36510>
- Folmer O, Black M, Hoeh W, Lutz R, Vrijenhoek R (1994) DNA primers for amplification of mitochondrial cytochrome *c* oxidase subunit I from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology* 3: 294–299.
- GBIF (2024) *Mycetomorpha* Potts, 1912. <https://doi.org/10.15468/dl.zkx9z3> [Accessed on 2024-02-05]
- Gurney RH, Grewe PM, Thresher RE (2006) Mitochondrial DNA haplotype variation in the parasitic cirripede *Sacculina carcini* observed in the cytochrome oxidase gene (COI). *Journal of Crustacean Biology* 26(3): 326–330. <https://doi.org/10.1651/S-2655.1>
- Høeg JT, Rybakov AV (1992) Revision of the Rhizocephala Akentrogonida (Cirripedia), with a list of all the species and a key to the identification of families. *Journal of Crustacean Biology* 12(4): 600–609. <https://doi.org/10.1163/193724092X00076>
- Høeg JT, Rybakov AV (1996) Development and taxonomy of the Mycetomorphidae and the significance of their reproductive system in rhizocephalan evolution (Crustacea: Cirripedia: Rhizocephala). *Zoologischer Anzeiger* 234: 253–269.
- Høeg JT, Rees DJ, Jensen PC, Glenner H (2019) Unravelling the evolutions of the Rhizocephala: a case study for molecular-based phylogeny in the parasitic Crustacea. In: Smit NJ, Bruce NL, Hadfield KA (Eds) *Parasitic Crustacea State of Knowledge and Future Trends*. Springer Nature Switzerland, Cham, 387–419. https://doi.org/10.1007/978-3-030-17385-2_9
- Høeg JT, Noever C, Rees DJ, Crandall KA, Glenner H (2020) A new molecular phylogeny-based taxonomy of parasitic barnacles (Crustacea: Cirripedia: Rhizocephala). *Zoological Journal of the Linnean Society* 190(2): 632–653. <https://doi.org/10.1093/zoolinnean/zlzl40>
- Jung J, Yoshida R, Lee D, Park J-K (2021) Morphological and molecular analyses of parasitic barnacles (Crustacea: Cirripedia: Rhizocephala) in Korea: preliminary data for the taxonomy and host ranges of Korean species. *PeerJ* 9: e12281. <https://doi.org/10.7717/peerj.12281>
- Kakui K, Hiruta C (2022) Description of a new *Hamatipeda* species, with an 18S molecular phylogeny (Crustacea: Tanaidacea: Tiphlotanidae). *Zoological Science* 39(1): 140–146. <https://doi.org/10.2108/zs210065>
- Kakui K, Shimada D (2017) A new species of *Tanaopsis* (Crustacea: Tanaidacea) from Japan, with remarks on the functions of serial ridges and grooves on the appendages. *Zootaxa* 4282(2): 324–336. <https://doi.org/10.11646/zootaxa.4282.2.6>
- Kakui K, Shimada D (2022) Dive into the sea: first molecular phylogenetic evidence of host expansion from terrestrial/freshwater to marine organisms in Mermithidae (Nematoda: Mermithida). *Journal of Helminthology* 96: e33. <https://doi.org/10.1017/S0022149X22000256>
- Kakui K, Katoh T, Hiruta SF, Kobayashi N, Kajihara H (2011) Molecular systematics of Tanaidacea (Crustacea: Peracarida) based on 18S sequence data, with an amendment of suborder/superfamily-level classification. *Zoological Science* 28(10): 749–757. <https://doi.org/10.2108/zsj.28.749>
- Kakui K, Fukuchi J, Shimada D (2021) First report of marine horsehair worms (Nematomorpha: *Nectonema*) parasitic in isopod crustaceans. *Parasitology Research* 120(7): 2357–2362. <https://doi.org/10.1007/s00436-021-07213-9>
- Kimura M (1980) A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* 16(2): 111–120. <https://doi.org/10.1007/BF01731581>
- Komai T (2012) A review of the western Pacific species of the crangonid genus *Metacrangon* Zarenkov, 1965 (Decapoda: Caridea), with descriptions of seven new species. *Zootaxa* 3468: 1–77. <https://doi.org/10.11646/zootaxa.3468.1.1>
- Komai T, Komatsu H (2009) Deep-sea shrimps and lobsters (Crustacea: Decapoda) from northern Japan, collected during the project “Research on deep-sea fauna and pollutants off Pacific coast of northern Japan”. *National Museum of Nature and Science Monograph* 39: 495–580.
- Korn OM, Golubinskaya DD, Rees DJ, Glenner H, Høeg JT (2020) Phylogenetic position, complete larval development and larval sexual dimorphism in a rhizocephalan barnacle, *Lernaeodiscus rybakovi* sp. nov. (Cirripedia: Rhizocephala: Peltogastridae), parasitizing the

- crab *Pachycheles stevensii* Stimpson, 1858 (Decapoda: Anomura: Porcellanidae). *Zoologischer Anzeiger* 287: 178–197. <https://doi.org/10.1016/j.jcz.2020.06.005>
- Kumar S, Stecher G, Tamura K (2016) MEGA7: Molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution* 33(7): 1870–1874. <https://doi.org/10.1093/molbev/msw054>
- Lockyer AE, Olson PD, Littlewood DTJ (2003) Utility of complete large and small subunit rRNA genes in resolving the phylogeny of the Neodermata (Platyhelminthes): Implications and a review of the cercomer theory. *Biological Journal of the Linnean Society. Linnean Society of London* 78(2): 155–171. <https://doi.org/10.1046/j.1095-8312.2003.00141.x>
- Nakayama T, Watanabe S, Mitsui K, Uchida H, Inouye I (1996) The phylogenetic relationship between the Chlamydomonadales and Chlorococcales inferred from 18SrDNA sequence data. *Phycological Research* 44(1): 47–55. <https://doi.org/10.1111/j.1440-1835.1996.tb00037.x>
- NOAA National Geophysical Data Center (2009) ETOPO1 1 Arc-Minute Global Relief Model. NOAA National Centers for Environmental Information. <https://www.ncei.noaa.gov/access/metadata/landing-page/bin/iso?id=gov.noaa.ngdc.mgg.dem:316> [Accessed on 2024-02-11]
- Noever C, Olson A, Glenner H (2016) Two new cryptic and sympatric species of the king crab parasite *Briarosaccus* (Cirripedia: Rhizocephala) in the North Pacific. *Zoological Journal of the Linnean Society* 176(1): 3–14. <https://doi.org/10.1111/zoj.12304>
- Orrell T, Informatics Office (2024) NMNH Extant Specimen Records (USNM, US). Version 1.77. National Museum of Natural History, Smithsonian Institution. Occurrence dataset. <https://doi.org/10.15468/hnhrg3> [Accessed via GBIF.org on 2024-02-05]
- Palumbi S, Martin A, Romano S, McMillan WO, Stice L, Grabowski G (2002) The simple fool's guide to PCR, version 2.0. <https://search-works.stanford.edu/view/9267895> [Accessed on 2024-02-08]
- Potts FA (1912) *Mycetomorpha*, a new rhizocephalan (with a note on the sexual condition of *Sylon*). *Zoologische Jahrbucher. Abteilung fur Systematik, Geographie und Biologie der Tiere* 33: 575–594. <https://doi.org/10.5962/bhl.part.17421>
- Rathbun MJ (1899) List of Crustacea known to occur on and near the Pribilof Islands. In: Jordan DS, Stejneger L, Lucas FA, Moser JF, Townsend CH, Clark GA, Murray J (Eds) *The Fur Seals and Fur-Seal Islands of the North Pacific Ocean, Part 3*. Government Printing Office, Washington, 555–557.
- Rathbun MJ (1902) Descriptions of new decapod crustaceans from the west coast of North America. *Proceedings of the United States National Museum* 24(1272): 885–905. <https://doi.org/10.5479/si.00963801.1272.885>
- Sloan NA, Bartier PM, Austin WC (2001) Living marine legacy of Gwaii Haanas. II: Marine invertebrate baseline to 2000 and invertebrate-related management issues. <https://doi.org/10.15468/9o6bjb> [Accessed via GBIF.org on 2024-02-05]
- Wessel P, Luis JF, Uieda L, Scharroo R, Wobbe F, Smith WHF, Tian D (2019) The generic mapping tools version 6. *Geochemistry, Geophysics, Geosystems* 20(11): 5556–5564. <https://doi.org/10.1029/2019GC008515>
- Wheeler E, McIntosh H (2021) Royal BC Museum—Invertebrates Collection. Version 1.2. Royal British Columbia Museum. Occurrence dataset. <https://doi.org/10.5886/zh7n1e> [Accessed via GBIF.org on 2024-02-05]
- Whiting MF (2002) Mecoptera is paraphyletic: Multiple genes and phylogeny of Mecoptera and Siphonaptera. *Zoologica Scripta* 31(1): 93–104. <https://doi.org/10.1046/j.0300-3256.2001.00095.x>